Amendments to the Claims

Claim 1 (Currently amended):   A method for modeling cellular metabolism of an

organism, comprising:

constructing a flux balance analysis model;

applying constraints to the flux balance analysis model, wherein the constraints ~~selected from the~~

~~set consisting of:~~ include qualitative kinetic information constraints~~, qualitative regulatory~~

~~information constraints, and differential DNA microarray experimental data constraints~~.

Claim 2 (Currently amended):   The method of claim 1 wherein the constraints ~~are~~ include

logic constraints selected to protect against violation of a kinetic ~~or regulatory~~ barrier.

Claim 3 (Currently amended):   The method of claim 1 wherein the constraints further

include a set of ~~are~~ connectivity restraints.

Claim 4 (Original):   The method of claim 1 further comprising the step of applying mixed-

integer linear programming to solve for a desired metabolic outcome.

Claim 5 (Original):   The method of claim 1 further comprising the step of solving for a desired

metabolic outcome.

Claim 6 (Original):   A method for modeling cellular metabolism of an organism that improves

upon a flux balance analysis model, comprising:

constructing the flux balance analysis model; and

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applying a plurality of logic constraints to the flux balance analysis model.

Claim 7 (Original):   The method of claim 6, further comprising selecting the set of logic constraints to protect against violation a kinetic or regulatory barrier.

Claim 8 (Original):   The method of claim 6 wherein the logic constraints are defined by a relationship between changes in reaction fluxes and metabolic concentrations.

Claim 9 (Withdrawn):   The method of claim 6 wherein the logic constraints are defined by a relationship between reaction fluxes and transcript levels of gene coding.

Claim 10 (Original):   The method of claim 6 wherein the logic constraints are represented by binary variables.

Claim 11 (Original):   The method of claim 10 wherein a first binary variable represents the presence of a reaction and a second binary variable represents the absence of a reaction.

Claim 12 (Original):   The method of claim 6 further comprising applying a computational procedure to identify a minimal set of metabolic reactions.

Claim 13 (Original):   The method of claim 12 further comprising selecting a growth rate, and wherein the step of applying a computational procedure is applying a computational procedure to identify the minimal set of metabolic reactions capable of supporting the growth rate.

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Claim 14 (Original): The method of claim 6 further comprising the step of applying mixed-integer linear programming to solve for a desired metabolic outcome.

Claim 15 (Original): The method of claim 6 further comprising the step of solving for a desired metabolic outcome.

Claim 16 (Original): The method of claim 15 further comprising engineering a change in an organism based on the desired metabolic outcome.

Claim 17 (Withdrawn):   A method for determining a reduced genome, comprising:

selecting a minimal set of reactions from a set of metabolic reactions that meets a growth rate
          target;

mapping enzymes catalyzing the minimal set of reactions to a corresponding set of coding genes,
          the corresponding set of coding genes defining a reduced genome.

Claim 18 (Withdrawn):   The method of claim 16 wherein the growth rate target is a biomass target production rate.

Claim 19 (Original): A system for modeling cellular metabolism of an organism, comprising:

a flux balance analysis model;

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a plurality of constraints applied to the flux balance analysis model, the constraints selected from

the set consisting of qualitative kinetic information constraints, qualitative regulatory

information constraints, and differential DNA microarray experimental data constraints.

Claim 20 (New):   The method of claim 1 wherein the constraints further include qualitative

regulatory information constraints.

Claim 21 (New):   The method of claim 20 wherein the constraints include logic constraints

selected to protect against violation of a regulatory barrier.

Claim 22 (New):   The system of claim 1 wherein the constraints further include DNA

experimental data constraints.

Claim 23 (New):   A method for modeling cellular metabolism of an organism, comprising:

constructing a flux balance analysis model;

applying constraints to the flux balance analysis model, wherein the constraints include

qualitative regulatory information constraints.

Claim 24 (New):   The method of claim 23 wherein the constraints include logic constraints

selected to protect against violation of a regulatory barrier.

Claim 25 (New):   The method of claim 23 wherein the constraints further include

connectivity restraints.

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Claim 26 (New):   The method of claim 23 further comprising applying mixed-integer linear

programming to solve for a desired metabolic outcome.

Claim 27 (New):   The method of claim 23 further comprising solving for a desired metabolic

outcome.

Claim 28 (New):   The method of claim 23 wherein the constraints further include differential

DNA microarray experimental data constraints.,

Claim 29 (New):   A method for modeling cellular metabolism of an organism, comprising:

constructing a flux balance analysis model;

applying constraints to the flux balance analysis model, wherein the constraints include

        differential DNA microarray experimental data constraints.

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